Replacement Sheet

SEQUENCE LISTING

<110> Farese, Robert V.
Cases, Sylvaine
Smith, Steven
Erickson, Sandra

<120> Diacylglycerol O-Acyltransferase

<130> 6510-105CIP2

<150> 60/107,771
<151> 1998-11-09

<150> PCT/US98/17883
<151> 1998-08-28

<150> 09/103,754
<151> 1998-06-24

<150> 09/339,472
<151> 1999-06-23

<160> 10

<170> FastSEQ for Windows Version 3.0

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<211> 1411
<212> DNA
<213> homo sapiens

<400> 1

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gcgggactgc tgctgcacgt ggccaacctg gccaccattc tgtgtttccc agcggctgtg 240
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<210> 2
<211> 261
<212> DNA
<213> homo sapiens

<400> 2
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tcctctggtc ccagggaggc ctctctgccc ctatggggct ctgtcctgca cccctcaggg     180
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<212> DNA
<213> mus musculus

<400> 3
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gctctcggcg tcggaggacc ggctcgcggg tttccgtcca gggtggtagt gggcccaagg     180
tagaagagga cgaggtgcga gacgcggctg tgagccccga cttgggcgcc gggggtgacg     240
cgccggctcc ggctccggct ccagcccata cccgggacaa agacgggcgg accagcgtgg     300
gcgacggcta ctgggatctg aggtgccatc gtctgcaaga ttctttgttc agctcagaca     360
gtggtttcag caattatcgt ggtatcctga attggtgtgt ggtgatgctg atcctgagta     420
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tggtgtctct gtttttgaag gaccccctaca gctggcctgc cccatgcgtg attattgcat     540
ccaatatttt tgttgtggct gcatttcaga ttgagaagcg cctggcagtg ggtgccctga     600
cagagcagat ggggctgctg ctacatgtgg ttaacctggc cacaatcatt tgcttcccag     660
cagctgtggc cttactggtt gagtctatca ctccagtggg ttccgtgttt gctctggcat     720
catactccat catgttcctc aagctttatt cctaccggga tgtcaacctg tggtgccgcc     780
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agcaagctgt gagctatcca gacaacctga cctaccgaga tctctattac ttcatctttg     900
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gcgagttcta cagagattgg tggaatgctg agtctgtcac ctacttttgg cagaactgga    1260
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gcagcaaatg ggtggccagg acaggagtat ttttgacctc agccttcttc catgagtacc    1380
tagtgagcgt tcccctgcgg atgttccgcc tctgggcatt cacagccatg atggctcagg    1440
tcccactggc ctggattgtg ggccgattct tccaagggaa ctatggcaat gcagctgtgt    1500
gggtgacact catcattggg caaccggtgg ctgtgctcat gtatgtccac gactactacg    1560
tgctcaacta cgatgcccca gtgggggtat gagctactgc caaaggccag ccctccctaa    1620
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<210> 4
<211> 629
<212> DNA
<213> arabidopsis thaliana

<220>
<221> misc_feature
<222> (0)...(0)
<223> Each n residue at position 455, 464, 467, 475, 497, 500, 508, 514, 519, 536, 543, 544, 576, 583, 584 and 597 can be either a, c, g or t

<400> 4
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attcatggga tttataatag aacaatatat aaatcctatt gtcaggaact caaagcatcc     120
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tttgaaaggc gatcttctat atgctattga aagagtgttg aagctttcag ttccaaattt 180
atatgtgtgg ctctgcatgt tctactgctt cttccacctt tggttaaaca tattggcaga 240
gcttctctgc ttcggggatc gtgaattcta caaagattgg tggaatgcaa aaagtgtggg 300
agattactgg gagaatgtgg aatatgcctg tccataaatg ggatgggtcc gacatatata 360
ccttcccgt gcttgcgcac aaggattacc caaagacacc ccggccatta accattggct 420
ttcccaagcc ccctggaggc ctttccatgg gccanggacc cggngtnccc tggcnggccc 480
ttcaaagcaa aggggngttn cctggggnta aagntccang ggcccttggg gcccanccaa 540
aannttcccc cgggaaaggg ttgcccaccg gggggngaaa aannccggg ggcaccncgg 600
aattttggga acccgggggg ggccttttt 629

<210> 5
<211> 386
<212> PRT
<213> homo sapiens

<400> 5
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Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala Pro
20 25 30
Cys Leu Val Ile Ala Ala Asn Val Phe Ala Val Ala Ala Phe Gln Val
35 40 45
Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala Gly Leu Leu
50 55 60
Leu His Val Ala Asn Leu Ala Thr Ile Leu Cys Phe Pro Ala Ala Val
65 70 75 80
Val Leu Leu Val Glu Ser Ile Thr Pro Val Gly Ser Leu Leu Ala Leu
85 90 95
Met Ala His Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr Arg Asp Val
100 105 110
Asn Ser Trp Cys Arg Arg Ala Arg Ala Lys Ala Ala Ser Ala Gly Lys
115 120 125
Lys Ala Ser Ser Val Ala Ala Pro His Thr Val Ser Tyr Pro Asp Asn
130 135 140
Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu Phe Ala Pro Thr Leu Cys
145 150 155 160
Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe Leu
165 170 175
Leu Arg Arg Ile Leu Glu Met Leu Phe Phe Thr Gln Leu Gln Val Gly
180 185 190
Leu Ile Gln Gln Trp Met Val Pro Thr Ile Gln Asn Ser Met Lys Pro
195 200 205
Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu Leu Lys Leu
210 215 220
Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Leu Phe
225 230 235 240
His Ser Cys Leu Asn Ala Val Ala Glu Leu Met Gln Phe Gly Asp Arg
245 250 255
Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser Val Thr Tyr Phe Trp
260 265 270
Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe Tyr
275 280 285
Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Met Ala Arg Thr Gly
290 295 300
Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val Ser Val Pro
305 310 315 320
Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met Met Ala Gln Ile
325 330 335
Pro Leu Ala Trp Phe Val Gly Arg Phe Phe Gln Gly Asn Tyr Gly Asn
340 345 350
Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro Ile Ala Val Leu

CONFIDENTIAL

355 360 365
Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Glu Ala Pro Ala Ala
370 375 380
Glu Ala
385

<210> 6
<211> 488
<212> PRT
<213> homo sapiens

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Asp Ala Ala Ala Gly Pro Asp Val Gly Ala Ala Gly Asp Ala Pro Ala
35 40 45
Pro Ala Pro Asn Lys Asp Gly Asp Ala Gly Val Gly Ser Gly His Trp
50 55 60
Glu Leu Arg Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser
65 70 75 80
Gly Phe Ser Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu
85 90 95
Ile Leu Ser Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly
100 105 110
Ile Leu Val Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro
115 120 125
His Ser Trp Pro Ala Pro Cys Leu Val Ile Ala Ala Asn Val Phe Ala
130 135 140
Val Ala Ala Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr
145 150 155 160
Glu Gln Ala Gly Leu Leu Leu His Val Ala Asn Leu Ala Thr Ile Leu
165 170 175
Cys Phe Pro Ala Ala Val Val Leu Leu Val Glu Ser Ile Thr Pro Val
180 185 190
Gly Ser Leu Leu Ala Leu Met Ala His Thr Ile Leu Phe Leu Lys Leu
195 200 205
Phe Ser Tyr Arg Asp Val Asn Ser Trp Cys Arg Arg Ala Arg Ala Lys
210 215 220
Ala Ala Ser Ala Gly Lys Lys Ala Ser Ser Ala Ala Ala Pro His Thr
225 230 235 240
Val Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu
245 250 255
Phe Ala Pro Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg
260 265 270
Ile Arg Lys Arg Phe Leu Leu Arg Arg Ile Leu Glu Met Leu Phe Phe
275 280 285
Thr Gln Leu Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile
290 295 300
Gln Asn Ser Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile
305 310 315 320
Glu Arg Leu Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile
325 330 335
Phe Phe Tyr Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu
340 345 350
Met Gln Phe Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu
355 360 365
Ser Val Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp
370 375 380
Cys Ile Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys

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Trp Met Ala Arg Thr Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu
                405                 410                 415
Tyr Leu Val Ser Val Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr
            420                 425                 430
Gly Met Met Ala Gln Ile Pro Leu Ala Trp Phe Val Gly Arg Phe Phe
        435                 440                 445
Gln Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly
    450                 455                 460
Gln Pro Ile Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn
465                 470                 475                 480
Tyr Glu Ala Pro Ala Ala Glu Ala
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<210> 7
<211> 498
<212> PRT
<213> mus musculus

<400> 7

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Glu Val Arg Asp Ala Ala Val Ser Pro Asp Leu Gly Ala Gly Gly Asp
        35                  40                  45
Ala Pro Ala Pro Ala Pro Ala Pro Ala His Thr Arg Asp Lys Asp Gly
    50                  55                  60
Arg Thr Ser Val Gly Asp Gly Tyr Trp Asp Leu Arg Cys His Arg Leu
65                  70                  75                  80
Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr Arg Gly
                85                  90                  95
Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala Arg Leu
            100                 105                 110
Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro Ile Gln
        115                 120                 125
Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala Pro Cys
    130                 135                 140
Val Ile Ile Ala Ser Asn Ile Phe Val Val Ala Ala Phe Gln Ile Glu
145                 150                 155                 160
Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Met Gly Leu Leu Leu
                165                 170                 175
His Val Val Asn Leu Ala Thr Ile Ile Cys Phe Pro Ala Ala Val Ala
            180                 185                 190
Leu Leu Val Glu Ser Ile Thr Pro Val Gly Ser Val Phe Ala Leu Ala
        195                 200                 205
Ser Tyr Ser Ile Met Phe Leu Lys Leu Tyr Ser Tyr Arg Asp Val Asn
    210                 215                 220
Leu Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser Thr Gly
225                 230                 235                 240
Lys Lys Val Ser Gly Ala Ala Ala Gln Gln Ala Val Ser Tyr Pro Asp
                245                 250                 255
Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro Thr Leu
            260                 265                 270
Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
        275                 280                 285
Leu Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu Gln Val
    290                 295                 300
Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile His Asn Ser Met Lys
305                 310                 315                 320
Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu Leu Lys
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Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Phe
            340                 345                 350
Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe Gly Asp
        355                 360                 365
Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr Tyr Phe
    370                 375                 380
Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe
385                 390                 395                 400
Tyr Lys Pro Met Leu Arg His Gly Ser Ser Lys Trp Val Ala Arg Thr
                405                 410                 415
Gly Val Phe Leu Thr Ser Ala Phe Phe His Glu Tyr Leu Val Ser Val
            420                 425                 430
Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met Ala Gln
        435                 440                 445
Val Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Gln Gly Asn Tyr Gly
    450                 455                 460
Asn Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val Ala Val
465                 470                 475                 480
Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala Pro Val
                485                 490                 495
Gly Val
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<210> 8
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<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide-FLAG epitope

<400> 8

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<211> 1650
<212> DNA
<213> mus musculus

<400> 9

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tagaagagga cgaggtgcga gacgcggctg tgagccccga cttgggcgcc gggggtgacg     240
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gcgacggcta ctgggatctg aggtgccatc gtctgcaaga ttcttttgttc agctcagaca     360
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ccaatatttt tgttgtggct gcatttcaga ttgagaagcg cctggcagtg ggtgccctga     600
cagagcagat ggggctgctg ctacatgtgg ttaacctggc cacaatcatt tgcttcccag     660
cagctgtggc cttactggtt gagtctatca ctccagtggg ttccgtgttt gctctggcat     720
catactccat catgttcctc aagctttatt cctaccggga tgtcaacctg tggtgccgcc     780
agcgaagggt caaggccaaa gctgtctcta cagggaagaa ggtcagtggg gctgctgccc     840
agcaagctgt gagctatcca gacaacctga cctaccgaga tctctattac ttcatctttg     900
ctcctacttt gtgttatgaa ctcaactttc ctcggtcccc cgcaatacga aagcgctttc     960
tgctacgacg agttcttgag atgctctttt ttacccagct tcaagtgggg ctgatccaac    1020
agtggatggt ccctactatc cacaactcca tgaagccctt caaggatatg gactattcac    1080
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TOSOH STECHNOT

FOR EXAMINATION

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tgctcaacta cgatgcccca gtgggggtat gagctactgc caaaggccag ccctccctaa   1620
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<210> 10
<211> 498
<212> PRT
<213> mus musculus

<400> 10

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            20                  25                  30
Glu Val Arg Asp Ala Ala Val Ser Pro Asp Leu Gly Ala Gly Gly Asp
        35                  40                  45
Ala Pro Ala Pro Ala Pro Ala Pro Ala His Thr Arg Asp Lys Asp Gly
    50                  55                  60
Arg Thr Ser Val Gly Asp Gly Tyr Trp Asp Leu Arg Cys His Arg Leu
65                  70                  75                  80
Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr Arg Gly
                85                  90                  95
Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala Arg Leu
            100                 105                 110
Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro Ile Gln
        115                 120                 125
Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala Pro Cys
    130                 135                 140
Val Ile Ile Ala Ser Asn Ile Phe Val Val Ala Ala Phe Gln Ile Glu
145                 150                 155                 160
Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Met Gly Leu Leu Leu
                165                 170                 175
His Val Val Asn Leu Ala Thr Ile Ile Cys Phe Pro Ala Ala Val Ala
            180                 185                 190
Leu Leu Val Glu Ser Ile Thr Pro Val Gly Ser Val Phe Ala Leu Ala
        195                 200                 205
Ser Tyr Ser Ile Met Phe Leu Lys Leu Tyr Ser Tyr Arg Asp Val Asn
    210                 215                 220
Leu Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser Thr Gly
225                 230                 235                 240
Lys Lys Val Ser Gly Ala Ala Ala Gln Gln Ala Val Ser Tyr Pro Asp
                245                 250                 255
Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro Thr Leu
            260                 265                 270
Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
        275                 280                 285
Leu Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu Gln Val
    290                 295                 300
Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile His Asn Ser Met Lys
305                 310                 315                 320
Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu Leu Lys
                325                 330                 335
Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Phe
            340                 345                 350
Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe Gly Asp
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        355                 360                 365
Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr Tyr Phe
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Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe
385                 390                 395                 400
Tyr Lys Pro Met Leu Arg His Gly Ser Ser Lys Trp Val Ala Arg Thr
                405                 410                 415
Gly Val Phe Leu Thr Ser Ala Phe Phe His Glu Tyr Leu Val Ser Val
            420                 425                 430
Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met Ala Gln
        435                 440                 445
Val Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Gln Gly Asn Tyr Gly
    450                 455                 460
Asn Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val Ala Val
465                 470                 475                 480
Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala Pro Val
                485                 490                 495
Gly Val
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